09/936,146.

```
=> s (oligo? or nucleo?) (5a) trans splic? (10a) 3(2a) exon?
L30          6 (OLIGO? OR NUCLEO?) (5A) TRANS SPLIC? (10A) 3(2A) EXON?

=> s l30 not l29
L31          6 L30 NOT L29

=> dup rem l31
PROCESSING COMPLETED FOR L31
L32           4 DUP REM L31 (2 DUPLICATES REMOVED)

=> d l32 1-4 bib abs

L32  ANSWER 1 OF 4  USPATFULL on STN
AN     2004:221289  USPATFULL
TI     Alteration of sequence of a target molecule
IN     Sullenger, Bruce, Westminster, CO, UNITED STATES
       Cech, Thomas, Boulder, CO, UNITED STATES
PI     US 2004171058      A1   20040902
AI     US 2004-799535     A1   20040312 (10)
RLI    Continuation of Ser. No. US 1998-165514, filed on 2 Oct 1998, ABANDONED
       Continuation of Ser. No. US 1997-786753, filed on 24 Jan 1997, GRANTED,
       Pat. No. US 5869254 Continuation of Ser. No. US 1993-152450, filed on 12
       Nov 1993, GRANTED, Pat. No. US 5667969
DT     Utility
FS     APPLICATION
LREP   Patrick G. Gattari, McDonnell Boehnen Hulbert & Berghoff, 32nd Floor,
       300 S. Wacker Drive, Chicago, IL, 60606
CLMN   Number of Claims: 12
ECL    Exemplary Claim: 1
DRWN   8 Drawing Page(s)
LN.CNT 993
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     Method for splicing a target nucleic acid molecule with a separate
       nucleic acid molecule. Such splicing generally causes production of a
       chimeric protein with advantageous features over that protein naturally
       produced from the target nucleic acid prior to splicing. The method
       includes contacting the target nucleic acid molecule with a catalytic
       nucleic acid molecule including the separate nucleic acid molecule. Such
       contacting is performed under conditions in which at least a portion of
       the separate nucleic acid molecule is spliced with at least a portion of
       the target nucleic acid molecule to form a chimeric nucleic acid
       molecule. In this method, the catalytic nucleic molecule is chosen so
       that it is not naturally associated with the separate nucleic acid
       molecule.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L32  ANSWER 2 OF 4  USPATFULL on STN
AN     1999:18925  USPATFULL
TI     Alteration of sequence of a target molecule by ribozyme catalyzed
       trans-splicing
IN     Sullenger, Bruce A., Westminster, CO, United States
       Cech, Thomas R., Boulder, CO, United States
PA     University Research Corporation, Boulder, CO, United States (U.S.
       corporation)
PI     US 5869254              19990209
AI     US 1997-786753          19970124 (8)
RLI    Continuation of Ser. No. US 1993-152450, filed on 12 Nov 1993, now
       patented, Pat. No. US 5667969
DT     Utility
FS     Granted
```

EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Fredman, Jeffrey
LREP Lyon & Lyon LLP
CLMN Number of Claims: 6
ECL Exemplary Claim: 2
DRWN 12 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 977
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Method for splicing a target nucleic acid molecule with a separate nucleic acid molecule. Such splicing generally causes production of a chimeric protein with advantageous features over that protein naturally produced from the target nucleic acid prior to splicing. The method includes contacting the target nucleic acid molecule with a catalytic nucleic acid molecule including the separate nucleic acid molecule. Such contacting is performed under conditions in which at least a portion of the separate nucleic acid molecule is spliced with at least a portion of the target nucleic acid molecule to form a chimeric nucleic acid molecule. In this method, the catalytic nucleic molecule is chosen so that it is not naturally associated with the separate nucleic acid molecule.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L32 ANSWER 3 OF 4 USPATFULL on STN
AN 97:83798 USPATFULL
TI Alteration of sequence of a deleterious target molecule by ribozyme catalyzed trans-splicing
IN Sullenger, Bruce A., Westminster, CO, United States
Cech, Thomas R., Boulder, CO, United States
PA University Research Corporation, Boulder, CO, United States (U.S. corporation)
PI US 5667969 19970916
AI US 1993-152450 19931112 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Zitomer, Stephanie W.; Assistant Examiner: Fredman, Jeffrey
LREP Lyon & Lyon
CLMN Number of Claims: 7
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 1006
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Method for splicing a target nucleic acid molecule with a separate nucleic acid molecule. Such splicing generally causes production of a chimeric protein with advantageous features over that protein naturally produced from the target nucleic acid prior to splicing. The method includes contacting the target nucleic acid molecule with a catalytic nucleic acid molecule including the separate nucleic acid molecule. Such contacting is performed under conditions in which at least a portion of the separate nucleic acid molecule is spliced with at least a portion of the target nucleic acid molecule to form a chimeric nucleic acid molecule. In this method, the catalytic nucleic molecule is chosen so that it is not naturally associated with the separate nucleic acid molecule.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L32 ANSWER 4 OF 4 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
DUPLICATE 1
AN 1993:73882 BIOSIS
DN PREV199395038382
TI Analysis of the Caenorhabditis elegans axonal guidance and outgrowth gene

unc-33.

AU Li, Wei; Herman, Robert K.; Shaw, Jocelyn E.
CS Dep. Genetics Cell Biol., Univ. Minn., St. Paul, Minnesota 55108, USA

SO Genetics, (1992) Vol. 132, No. 3, pp. 675-689.
CODEN: GENTAE. ISSN: 0016-6731.
DT Article
LA English
ED Entered STN: 26 Jan 1993
Last Updated on STN: 26 Jan 1993

AB Mutations in the unc-33 gene of the nematode Caenorhabditis elegans lead to severely uncoordinated movement, abnormalities in the guidance and outgrowth of the axons of many neurons, and a superabundance of microtubules in neuronal processes. We have cloned unc-33 by tagging the gene with the transposable element Tc4. Three unc-33 messages, which are transcribed from a genomic region of at least 10 kb, were identified and characterized. The three messages have common 3' ends and identical reading frames. The largest (3.8-kb) message consists of the 22-**nucleotide trans-spliced** leader SL1 and 10 **exons** (I-X); the intermediate-size (**3**.3-kb) message begins with SL1 spliced to the 5' end of exon V and includes exons V-X; and the smallest (2.8-kb) message begins within exon VII and also includes exons VIII-X. A gamma-ray-induced deletion mutation situated within exon VIII reduces the sizes of all three messages by 0.5 kb. The three putative polypeptides encoded by the three messages overlap in C-terminal sequence but differ by the positions at which their N termini begin; none has significant similarity to any other known protein. A Tc4 insertion in exon VII leads to alterations in splicing that result in three approximately wild-type-size messages: the Tc4 sequence and 28 additional nucleotides are spliced out of the two larger messages; the Tc4 sequence is trans-spliced off the smallest message such that SL1 is added 13 nucleotides upstream of the normal 5' end of the smallest message.